## Effect of Natural Selection and Genetic Drift in differences of allele frequencies between populations of *Cepaea nemoralis*.

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In this module we have been looking at polymorphism, genetic variances within members of the same populations, and the processes that contribute to its establishment and maintenance: natural selection, sexual selection, gene flow, and/or genetic drift. By acquiring evidence from field work, statistical analysis of data and phenotypic/genotypic specimen analysis, we can gain a deeper understanding of how these processes work and interact with each other.

**Box 1. Null and Alternative Hypotheses.**

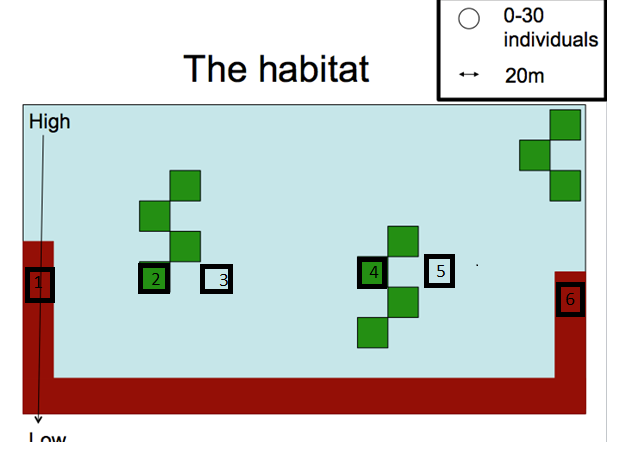
**H0**: There is no obvious, clear correlation between the distribution and frequency of specific shell phenotypes and defined habitats of different independent populations of *Cepaea nemoralis,* assuming negligible gene flow between distant populations.

**H1**: There is an obvious, clear correlation between the distribution and frequency of specific shell phenotypes and defined habitat of different independent populations of *Cepaea nemoralis,* assuming negligible gene flow between distant populations.

In our experiment we will attempt to determine the effects of these evolutionary processes in the differences in allele frequencies between different populations of *Cepaea nemoralis* (**Box 1**.)by measuring and comparing the frequency and distribution of individual shell phenotypes across a range of different habitats (**Figure 1.**) Our aim is to explain the origin of polymorphism (the raw material for evolution and differentiation) in these populations of *Cepaea nemoralis* and to theorize how our design and results could be implemented to the study of polymorphism other species.

Previous experiments (**Jones et al. 1977**) which attempted to explain the reasons behind polymorphism in two similar snail species, *Cepaea nemoralis* and *Cepaea hortensis* concluded that it was not just the genetic drift but rather the combination of several different evolutionary processes and selective pressures that played a significant role in establishing polymorphism. Some of these factors were **visual selection by predator**, **climatic selection**, **frequency dependent selection**, **density dependent selection**, **heterozygote advantage** and **stabilizing selection**. Researchers were unable to infer a general rule that could explain polymorphism in all populations. Instead, results suggested that these factors had different effects which gave rise to polymorphism within each population. Our experiment lies in the background of such previous research conducted on *Cepaea* species trying to find a common ground for biologists to understand polymorphism and its role in evolution. Such issue is of great importance within the broad realm of Biology and specifically within the fields of Evolutionary and Population Genetics and Ecology.

When a certain species is found in a particular geographical area, and is capable of interbreeding, it is considered a population. Natural selection is the process where an allele gradually becomes more or less common in a population, while Genetic drift, on the other hand, is the random frequency change of an allele in a population and Gene flow is the introduction of alleles or genes from one population to another.



***Figure 1*** *- Schematic representation of the habitat. Squares 1 to 6 represent homogenous 25m ² quadrats areas where snails will be collected. Red colored areas represent woodland while green squares represent bush areas and background represents open grassland.*

In order to carry out our experiment and test our hypothesis (**Box 1.**), we will be collecting snails indiscriminately, both dead and alive, from six different areas across the field (**Figure 1**). Differences in shell colour and number of bands will be recorded and compared to all other areas. We have chosen areas at a relatively middle height to attempt to control for variables altitude and humidity. Based on previous work about the dispersal distances of land snails (**Aubry et al. 2006**) and assuming no significant dispersion over successive generations (and thus no significant gene flow), the collecting areas will be about 20 m apart to allow for observations to be safely independent and avoid pseudo replication. We aim to collect a total between 140-160 snails. Data obtained will be statistically analyzed to detect any sampling variations that could affect the results and conclusions.

By comparing the shells of these snails across different habitats we are effectively comparing their genotypes, just by observing their phenotypes, which is why *Cepaea nemoralis* is the organism in question within this experiment, since it can be easily be used as a model to explain the causes of polymorphism from which results could be extrapolated to other species, including Humans.